REMARKS

In an effort to expedite favorable prosecution, Applicants provide the following remarks premised on the Official Action issued in parent application serial no. 09/872,881 on November 19, 2002.

In that rejection, the Examiner rejected claims 1-2 and 13-16 (now 17-18 and 29-32) under 35 U.S.C. §103(a) over Carr (European Application Publication No. 0246864) in view of Cantor et al. (U.S. Patent No. 6,007,987). The Examiner admits that "Carr does not teach a probe with a double-stranded flag containing 4 units (SD, D0, D1 and ED) each having an arbitrary sequence bound to each other sequentially in the order mentioned and a marker substance".[1] The Examiner also again admits that Carr does not teach the multiplexing of detecting or quantifying a target nucleic acid having a predetermined sequence in a specimen with multiple probes A1-An and B1-Bn. Cantor et al. is then applied to allegedly remedy the admitted deficiencies of Carr.

Cantor et al. teach an array of R^4 different nucleic acid probes wherein each probe comprises a double-stranded portion of length D, a terminal single-stranded portion of length S, and a random nucleotide sequence within the single-stranded portion of length R (column 4, lines 8-17). From this, Applicants submit that the probe taught by Cantor et al. is formed of two or three units not formed of four units, as presently claimed. The expression "R^4 different nucleic acid probes" means that the types of random nucleic acid sequence of a probe may vary R^4 ways (actually R^4 appears to be a typographical error for 4^R).

[1] This concession is repeated from the first Official Action dated April 19, 2002 in the parent application 09/872,881 (See page 5).

Cantor et al. disclose "a set of nucleic acid probes wherein each probe has a double-stranded portion, a single-stranded portion, and a random sequence within the single-stranded portion" (in column 7, lines 11 to 14) and "if the random portion consisted of a four nucleotide sequence (R=4), the total number of possible combinations would be 44" (in column 7, lines 35 to 42). Cantor et al. further disclose "4^R different probes representing every member of the random sequence of length R, but arrays of less than 4^R are also encompassed by the invention" (in column 13, lines 6 and 7). The disclosures above are concerned with the length R and nothing to do with a probe that has 4 units; a clear teaching away from the claimed invention. Cantor et al. disclose that a probe is hybridized with a single-stranded nucleic acid. The portion R is single-stranded.

Therefore, nowhere do the references teach or suggest a flag having four units of SD, D0, D1 and ED. More specifically, the references do not even recognize a probe having a double-stranded flag in which individual units are mutually linked in the order mentioned via a sequence between them. Furthermore, Cantor et al. teach that preferable thermodynamic conditions are produced by the presence of a double-stranded portion, thereby accelerating hybridization.

Notably, the present invention is directed to using a probe having a double-stranded flag comprising 4 units, SD, D0, D1 and ED. Of the four units, the middle two units are used for encoding (recognizing) and the sequences at both ends are only employed for amplifying the probe by a PCR.

Accordingly, the four units contained in the flag of the present invention cannot only be amplified but can also encode the sequence which has been hybridized by the use of two of the four units. Furthermore, the probe of the present invention comprises a flag having 4 units

and a complementary sequence to a target nucleic acid sequence. The flag portion is not hybridized with the target nucleic acid sequence.

Thus, the probe of the present invention has a complimentary sequence S' in addition to the 4 units mentioned above. In this respect, the probe of the present invention clearly differs from and is not suggested by that disclosed by the combination of Carr and Cantor et al.

Applicants further submit that even if the probe of Cantor et al. is combined with the invention of Carr, it is impossible to reach the encoding method and amplification contemplated by use of the flag portion of the present invention. Therefore, the present invention is not suggested by these references.

Cleuziat et al. teach transcription of a single-stranded nucleic acid using two primers. However, the present invention is directed to a method of extending two complimentary chains simultaneously from a single nucleic acid. Therefore, the amplification method of Cleuziat et al. completely differs from the method of the present invention.

The present invention does not reside in amplification steps performed by the use of the transcription of a single-stranded nucleic acid. In the method of the present invention, a target nucleic acid is not amplified, but a flag sequence is amplified (called the encode reaction) only when a target nucleic acid is present. When the encode reaction is performed, the presence of the target nucleic acid is obtained as the information exhibited by the combination of D0n-D1n of the flag (formed of an orthonormal nucleotide sequence). Subsequently, by detecting the nucleic acid corresponding to the flag sequence obtained by the decode reaction, a target nucleic acid is detected or quantified. The PCR amplification is only used as a means for performing an encode reaction and a decode reaction.

Thus, a feature of the present invention resides in the detection of a target nucleic acid by encode and decode reactions.

From the foregoing, it is clear that even if the flag sequence having 4 units is combined with the inventions of Carr, Cantor, and Cleuziat, it is impossible to achieve the present invention. Therefore, the present invention is not suggested by these references.

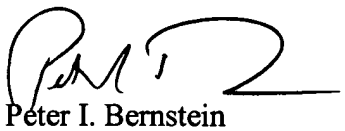
The Examiner also previously rejected claims 1-9 and 13-16 (now 17-28 and 29-32) as allegedly unpatentable over the combination of Carr in view of Cantor et al. and Wong (U.S. Patent No. 5,935,793).

The prima-facie rejection of the present invention based on Wong's invention directed to the hybridization of a tag sequence Tg with a complimentary tag sequence Tg' in view of Carr and Cantor et al. has been overcome by the amendment of the claims. The present invention is not suggested by Carr in combination with Cantor as described above. Therefore, if Wong is further combined to the references, the present invention cannot be suggested.

Accordingly, the pending claims are neither taught nor suggested by the previously cited references.

Wherefore, early and favorable consideration of the present application, as amended herein, is respectfully requested.

Respectfully submitted,



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